1631

RAW SEQUENCE LISTING   DATE: 07/06/2000
PATENT APPLICATION: US/09/233,218A   TIME: 13:06:42

Input Set : A:\Tetrapyrole-15090-B.txt
Output Set: N:\CRF3\07062000\I233218A.raw

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 1 <110> APPLICANT: CaJacob, Claire A.
 2       Liu, Jingdong
 4 <120> TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 5       The Tetrapyrrole Pathway
 7 <130> FILE REFERENCE: 38-21(15090)B
 9 <140> CURRENT APPLICATION NUMBER: US 09/233,218A
10 <141> CURRENT FILING DATE: 1999-01-20
12 <150> PRIOR APPLICATION NUMBER: US 60/067,000
13 <151> PRIOR FILING DATE: 1997-11-24
15 <150> PRIOR APPLICATION NUMBER: US 60/069,472
16 <151> PRIOR FILING DATE: 1997-12-09
18 <150> PRIOR APPLICATION NUMBER: US 60/072,027
19 <151> PRIOR FILING DATE: 1998-01-21
21 <150> PRIOR APPLICATION NUMBER: US 60/074,201
22 <151> PRIOR FILING DATE: 1998-02-10
24 <150> PRIOR APPLICATION NUMBER: US 60/074,282
25 <151> PRIOR FILING DATE: 1998-02-10
27 <150> PRIOR APPLICATION NUMBER: US 60/074,280
28 <151> PRIOR FILING DATE: 1998-02-10
30 <150> PRIOR APPLICATION NUMBER: US 60/074,281
31 <151> PRIOR FILING DATE: 1998-02-10
33 <150> PRIOR APPLICATION NUMBER: US 60/074,566
34 <151> PRIOR FILING DATE: 1998-02-12
36 <150> PRIOR APPLICATION NUMBER: US 60/074,567
37 <151> PRIOR FILING DATE: 1998-02-12
39 <150> PRIOR APPLICATION NUMBER: US 60/074,565
40 <151> PRIOR FILING DATE: 1998-02-12
42 <150> PRIOR APPLICATION NUMBER: US 60/075,462
43 <151> PRIOR FILING DATE: 1998-02-19
45 <150> PRIOR APPLICATION NUMBER: US 60/075,459
46 <151> PRIOR FILING DATE: 1998-02-19
48 <150> PRIOR APPLICATION NUMBER: US 60/075,461
49 <151> PRIOR FILING DATE: 1998-02-19
51 <150> PRIOR APPLICATION NUMBER: US 60/075,464
52 <151> PRIOR FILING DATE: 1998-02-19
54 <150> PRIOR APPLICATION NUMBER: US 60/075,460
55 <151> PRIOR FILING DATE: 1998-02-19
57 <150> PRIOR APPLICATION NUMBER: US 60/075,463
58 <151> PRIOR FILING DATE: 1998-02-19
60 <150> PRIOR APPLICATION NUMBER: US 60/077,231
61 <151> PRIOR FILING DATE: 1998-03-09
63 <150> PRIOR APPLICATION NUMBER: US 60/077,229
64 <151> PRIOR FILING DATE: 1998-03-09
66 <150> PRIOR APPLICATION NUMBER: US 60/077,230
67 <151> PRIOR FILING DATE: 1998-03-09
70 <151> PRIOR FILING DATE: 1998-03-18
73 <151> PRIOR FILING DATE: 1998-04-07
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ENTERED

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RAW SEQUENCE LISTING              DATE: 07/06/2000
PATENT APPLICATION:  US/09/233,218A    TIME: 13:06:42

Input Set : A:\Tetrapyrole-15090-B.txt
Output Set: N:\CRF3\07062000\I233218A.raw
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 76 <151> PRIOR FILING DATE: 1998-04-27
 79 <151> PRIOR FILING DATE: 1998-04-29
 82 <151> PRIOR FILING DATE: 1998-04-29
 85 <151> PRIOR FILING DATE: 1998-04-29
 88 <151> PRIOR FILING DATE: 1998-05-13
 91 <151> PRIOR FILING DATE: 1998-05-13
 94 <151> PRIOR FILING DATE: 1998-05-13
 97 <151> PRIOR FILING DATE: 1998-05-21
100 <151> PRIOR FILING DATE:. 1998-05-21
103 <151> PRIOR FILING DATE: 1998-05-21
106 <151> PRIOR FILING DATE: 1998-05-21
109 <151> PRIOR FILING DATE: 1998-05-21
112 <151> PRIOR FILING DATE: 1998-05-21
115 <151> PRIOR FILING DATE: 1998-06-16
118 <151> PRIOR FILING DATE: 1998-06-18
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124 <151> PRIOR FILING DATE: 1998-06-29
127 <151> PRIOR FILING DATE: 1998-06-30
130 <151> PRIOR FILING DATE: 1998-06-30
133 <151> PRIOR FILING DATE: 1998-09-09
136 <151> PRIOR FILING DATE: 1998-09-09
139 <151> PRIOR FILING DATE: 1998-09-16
142 <151> PRIOR FILING DATE: 1998-09-16
145 <151> PRIOR FILING DATE: 1998-09-21
148 <151> PRIOR FILING DATE: 1998-09-22
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154 <151> PRIOR FILING DATE: 1998-09-22
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166 <151> PRIOR FILING DATE: 1998-11-18
169 <151> PRIOR FILING DATE: 1998-11-18
172 <151> PRIOR FILING DATE: 1998-11-24
175 <151> PRIOR FILING DATE: 1998-12-08
178 <151> PRIOR FILING DATE: 1998-12-11
181 <151> PRIOR FILING DATE: 1998-12-22
183 <160> NUMBER OF SEQ ID NOS: 677
185 <210> SEQ ID NO: 1
186 <211> LENGTH: 257
187 <212> TYPE: DNA
188 <213> ORGANISM: Glycine max
190 <400> SEQUENCE: 1
192 tgctgcttct ggaaattttc attggaattt tgaagatgtt gctaaatcaa ttgtgtgcat    60
194 gatgatgtct ggcccattct tgacaggata tacccagact atgaatgatt ggtacgaccg   120
196 agaaattgat gcaataaatg aaccttatag accaattcct tctggggcaa tatctgagaa   180
198 tgaggtaatc actcaaatat gggtgttgct gcttggtggt ctttctctgg ctggtatatt   240
200 ggacatatgg gcagggc                                                  257
203 <210> SEQ ID NO: 2
204 <211> LENGTH: 272
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                    RAW SEQUENCE LISTING               DATE: 07/06/2000
                    PATENT APPLICATION:  US/09/233,218A       TIME: 13:06:42

                    Input Set : A:\Tetrapyrole-15090-B.txt
                    Output Set: N:\CRF3\07062000\I233218A.raw


        205 <212> TYPE: DNA
        206 <213> ORGANISM: Glycine max
        208 <223> OTHER INFORMATION: unsure at all n locations
W--> 209 <400> SEQUENCE: 2
        211 cacatgtaag catctcaagc tctgctgaat cttcaatggc ttctctactc aacatggttt   60
W--> 213 ctgttccatc aagaatatca ccaagctcac acacgagaac cacttcaang caatctcgaa  120
        215 ctgttttgcc accattttct gtctcatttt ccaggaggag attatcaatt agagcaacag  180
        217 aaactgatac taatgaagtt caatctcagg cgccgggtac agcaccatca aaagatggtt  240
        219 caagcttcaa ccagctcctt ggtattaaag ga                                272
        222 <210> SEQ ID NO: 3
        223 <211> LENGTH: 156
        224 <212> TYPE: DNA
        225 <213> ORGANISM: Glycine max
        227 <400> SEQUENCE: 3
        229 aagaaacaaa taagtggaag attcgtcttc aacttacaaa gccagtcact tggcctccat   60
        231 taatttgggg tgtagtttgt ggagctgctg cttctggaaa ttttcattgg aattttgaga  120
        233 tgttgctaaa tcaattgtgt gcatgatgat gtctgg                            156
        236 <210> SEQ ID NO: 4
        237 <211> LENGTH: 348
        238 <212> TYPE: DNA
        239 <213> ORGANISM: Glycine max
        241 <400> SEQUENCE: 4
        243 agtacggctg cgagaagacg acagaagggg aaggcatctt caagctctga atctgcaatg   60
        245 gcttctctac tcaacatggt ttcggttcca ccaagaatat caccaacctc acacaccaga  120
        247 atcgcttcgc ttcaagctcg acccgttttg ccaccctttt ctgtctcatt ttccaggagg  180
        249 agactatcaa ttagagcaac agaaactgat accaatgaag ttcaatctca ggcaccgggt  240
        251 gcagcgccat ctaaagatgg ttcaagcttc aatcagcttc ttggtatcaa aggagctgcc  300
        253 caagaaacaa ataaatggaa aattcgtctt caactcacaa agcctgtc                348
        256 <210> SEQ ID NO: 5
        257 <211> LENGTH: 245
        258 <212> TYPE: DNA
        259 <213> ORGANISM: Glycine max
        261 <223> OTHER INFORMATION: unsure at all n locations
W--> 262 <400> SEQUENCE: 5
W--> 264 ctctgaatct gcaatggctt ctctactcaa catggtttcg gttncaccaa gactatcact   60
W--> 266 cnnctcacac accagaatcg cttcgcttca agctcgaccc gtttgccacc cttttctgtc  120
        268 tcattttcca ggaggagact atcaattaga gcaacagaaa ctgataccaa tgaagttcaa  180
        270 tctcaggcac cgggtgcagc gccatctaaa gatggttcaa gcttcaatca gcttcttggt  240
        272 atcaa                                                             245
        275 <210> SEQ ID NO: 6
        276 <211> LENGTH: 268
        277 <212> TYPE: DNA
        278 <213> ORGANISM: Glycine max
        280 <400> SEQUENCE: 6
        282 tggcatcttc aagctctgaa tctgcaatgg cttctctact caacatggtt tcggttccac   60
        284 caagaatatc accaacctca cacaccagaa tcgcttcgct tcaagctcga cccgttttgc  120
        286 cacccttttc tgtctcattt tccaggagga gactatcaat tagagcaaca gaaactgata  180
        288 ccaatgaagt tcaatctcag gcaccgggtg cagcgccatc taaagatggt tcaagcttca  240
        290 atcagcttct tggtatcaaa ggagctgc                                    268
```

RAW SEQUENCE LISTING   DATE: 07/06/2000
PATENT APPLICATION: US/09/233,218A   TIME: 13:06:42

Input Set : A:\Tetrapyrole-15090-B.txt
Output Set: N:\CRF3\07062000\I233218A.raw

```
293 <210> SEQ ID NO: 7
294 <211> LENGTH: 278
295 <212> TYPE: DNA
296 <213> ORGANISM: Glycine max
298 <400> SEQUENCE: 7
300 cggctgcgag aagacgacag aagggctcag agtactgtta ttgaaaggca aaggacaata   60
302 gagtatacct gaagccctag agccctatcc ccttcaacac ttttgaagtc attgacaata  120
304 gcaattccca actgcaatgt gatttaacaa caacattaat aaccattttt atttgacata  180
306 ttatcatatt catatccaac aaaatgtcat gaagaatata ttacatactc cagctatgct  240
308 gtataggagt gtgagaacaa ttatatctgg tgtaagag                          278
311 <210> SEQ ID NO: 8
312 <211> LENGTH: 248
313 <212> TYPE: DNA
314 <213> ORGANISM: Glycine max
316 <400> SEQUENCE: 8
318 cggctgcgag aagacgacag aagggctcag agtactgtta ttgaaaggca aaggacaata   60
320 gagtatacct gaagccctag agccctatcc ccttcaacac ttttgaagtc attgacaata  120
322 gcaattccca actgcaatgt gatttaacaa caacattaat aaccattttt atttgacata  180
324 ttatcatatt catatccaac aaaatgtcat gaagaatata ttacatactc cagctatgct  240
326 gtatagga                                                           248
329 <210> SEQ ID NO: 9
330 <211> LENGTH: 258
331 <212> TYPE: DNA
332 <213> ORGANISM: Glycine max
334 <223> OTHER INFORMATION: unsure at all n locations
W--> 335 <400> SEQUENCE: 9
W--> 337 gncanctgct anggancta cntncactgg cngagggctt tgaacttagc ctnnnggaca   60
W--> 339 aatcatctng ggcatttcct cctctcgcgc cngttgctng aggacttgga naaatncgag  120
W--> 341 tacccttcaa aggcttgatn atcgtaggnt cacacgacag ggnacacaaa cacattggct  180
W--> 343 ggtaatgtac ctcccaaggc gaaccttggn ggacttgagg ggacttcagg gtggtttgaa  240
345 tgggctaaag agctcagc                                                258
348 <210> SEQ ID NO: 10
349 <211> LENGTH: 270
350 <212> TYPE: DNA
351 <213> ORGANISM: Glycine max
353 <400> SEQUENCE: 10
355 gtcaatttgt tgataacttt aggcaatcag gccggccact ggatgtgctt gtttgcaatg   60
357 ctgcggttta cttgccaact gccagggaac ctacatatac tgctgatggc tttgaactca  120
359 gtgttggaac caaccatctc gggcatttcc tcctttcgcg ccttttgctt gacgacttga  180
361 acaaatctga ctacccttcg aagcggttga tcatgtaggc tcaatcacag gaaacaccaa  240
363 cacattggct ggaatgtgcc acccaggcta                                   270
366 <210> SEQ ID NO: 11
367 <211> LENGTH: 258
368 <212> TYPE: DNA
369 <213> ORGANISM: Glycine max
371 <223> OTHER INFORMATION: unsure at all n locations
W--> 372 <400> SEQUENCE: 11
374 caggaaacac caacacattg gctggaaatg tgccacccaa ggctaacctt ggtgacatga   60
376 ggggactagc tggaggcttg aatgggctaa acacttcagc catgatagat ggaggatcct  120
```

```
                RAW SEQUENCE LISTING            DATE: 07/06/2000
                PATENT APPLICATION:  US/09/233,218A     TIME: 13:06:42

                Input Set : A:\Tetrapyrole-15090-B.txt
                Output Set: N:\CRF3\07062000\I233218A.raw


      378 ttgacggcgc taaggcatac aaggacagca aagtctgcaa catgcttaca atgccagaat   180
W--> 380 tccaacagga ggtcccngtt ganaccnngg natnacatnt gcncccntan cccngggttn   240
W--> 382 ttcncccaaa ngggnttt                                                 258
      385 <210> SEQ ID NO: 12
      386 <211> LENGTH: 270
      387 <212> TYPE: DNA
      388 <213> ORGANISM: Glycine max
      390 <400> SEQUENCE: 12
      392 gacggcgcta aggcatacaa ggacagcaaa gtctgcaaca tgcttacaat gcaagaattc    60
      394 cacagaagat accatgatga aactgggatc acatttgctt ccctttaccc aggttgcatc   120
      396 gccacaacag gcttgttcag agagcacatt cccttgttca gacttctctt ccctccattc   180
      398 caaaagtaca taaccaaggg ctttgtctca gaagatgaat caggaaagag acttgcacag   240
      400 gttgtgagtg atccaagcct aacaaaatca                                     270
      403 <210> SEQ ID NO: 13
      404 <211> LENGTH: 262
      405 <212> TYPE: DNA
      406 <213> ORGANISM: Glycine max
      408 <400> SEQUENCE: 13
      410 caggctgctt ctttccccat tgctaaagag ggaaagtctg gtgtttctct caggtacacc    60
      412 acaatgttcg gtgtttcatt gtcggatact ctcaaatctg acgctcagct tttcctcatt   120
      414 gacatgcaaa gaaacaccaa caccttggct ggacatgtgc cacccaaggc taaccttggt   180
      416 gacttgaggg gactagctgg aggcttgaat gggctaaaca cttcagccat gatagatgga   240
      418 ggatcctttg atggcaccaa gg                                             262
      421 <210> SEQ ID NO: 14
      422 <211> LENGTH: 279
      423 <212> TYPE: DNA
      424 <213> ORGANISM: Glycine max
      426 <223> OTHER INFORMATION: unsure at all n locations
W--> 427 <400> SEQUENCE: 14
      429 ccatttgctt ccctttaccc cggttgcatt gccacaacag gcctgttcag agagcacatt    60
W--> 431 cccttgttca naactctgtt ccctccattc cagaagtaca taaccaaagg ctatgtctca   120
      433 gaagatgaag caggaaagag acttgctcag gttgtaagtg atccaagcct aacaaaatct   180
      435 ggtgtttact ggagctgaa caaagcatca gcttcgtttg aaaaccagtt gtctcaggag   240
W--> 437 gccagtgata cagagaaggc tcgtaagatc tgggagnta                           279
      440 <210> SEQ ID NO: 15
      441 <211> LENGTH: 346
      442 <212> TYPE: DNA
      443 <213> ORGANISM: Glycine max
      445 <400> SEQUENCE: 15
      447 aaacaaagga cccagtttta catttttttt tgttcctgag ttccaatggc tcttcaggct    60
      449 gcttccttgg tttctgcttc tttttctatt gctaaagagg gaaagtctgg tgtatctctc   120
      451 agggacacca caatgtttgg tgtttcattg tcggatactc tcaaatctga cttcagctct   180
      453 ccctcatcga cttgcaaaag ggaattccaa caaaaatttg gccctttgag ggttcagtca   240
      455 gtggcaacaa caactccagg agtcaccaag gcttcaccag aaggcaagaa aactttgagg   300
      457 aaaggcagtg ttattatcac tggggcttcc tctggattag ctggc                    346
      460 <210> SEQ ID NO: 16
      461 <211> LENGTH: 256
      462 <212> TYPE: DNA
      463 <213> ORGANISM: Glycine max
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Please Note:
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n   r Xaa.**

```
              VERIFICATION SUMMARY                DATE: 07/06/2000
              PATENT APPLICATION:  US/09/233,218A    TIME: 13:06:43

              Input Set : A:\Tetrapyrole-15090-B.txt
              Output Set: N:\CRF3\07062000\I233218A.raw

L:69 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:72 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:75 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:78 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:81 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:84 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:87 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:90 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:93 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:96 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:99 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:102 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:105 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:108 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:111 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:114 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:117 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:120 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:123 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:126 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:129 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:132 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:135 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:138 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:141 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:144 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:147 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:150 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:153 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:156 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:159 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:162 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:165 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:168 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:171 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:174 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:177 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:180 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
L:209 M:283 W: Missing Blank Line separator, <400> field identifier
L:213 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:213 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:213 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:213 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:262 M:283 W: Missing Blank Line separator, <400> field identifier
L:264 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:264 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:264 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:264 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
```

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                    VERIFICATION SUMMARY              DATE: 07/06/2000
                    PATENT APPLICATION:  US/09/233,218A    TIME: 13:06:43

                    Input Set : A:\Tetrapyrole-15090-B.txt
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L:266 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:266 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:266 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
M:340 Repeated in SeqNo=5
L:335 M:283 W: Missing Blank Line separator, <400> field identifier
L:337 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
L:337 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:337 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:337 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
L:339 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
L:339 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:339 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
M:340 Repeated in SeqNo=9
L:341 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
L:341 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:341 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:343 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
L:343 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:343 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:372 M:283 W: Missing Blank Line separator, <400> field identifier
L:380 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:380 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:380 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:380 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
L:382 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:382 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:382 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
M:340 Repeated in SeqNo=11
L:427 M:283 W: Missing Blank Line separator, <400> field identifier
L:431 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:14
L:431 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:14
L:431 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
L:431 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
L:437 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:14
L:437 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:14
L:437 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
M:340 Repeated in SeqNo=14
L:502 M:283 W: Missing Blank Line separator, <400> field identifier
L:504 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:18
L:504 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18
L:504 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18
L:504 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
L:514 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:18
L:514 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18
L:514 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18
M:340 Repeated in SeqNo=18
L:685 M:283 W: Missing Blank Line separator, <400> field identifier
L:691 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:28
L:691 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
```

VERIFICATION SUMMARY   DATE: 07/06/2000
PATENT APPLICATION: US/09/233,218A   TIME: 13:06:43

Input Set : A:\Tetrapyrole-15090-B.txt
Output Set: N:\CRF3\07062000\I233218A.raw

L:691 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:691 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
L:693 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:28
L:693 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
L:693 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
M:340 Repeated in SeqNo=28
L:695 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:28
L:695 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
L:695 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:704 M:283 W: Missing Blank Line separator, <400> field identifier
L:706 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:29
L:706 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
L:706 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:29
M:340 Repeated in SeqNo=29
L:739 M:283 W: Missing Blank Line separator, <400> field identifier
L:755 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:31
L:782 M:283 W: Missing Blank Line separator, <400> field identifier
L:790 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:33
L:815 M:283 W: Missing Blank Line separator, <400> field identifier
L:817 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:35
L:834 M:283 W: Missing Blank Line separator, <400> field identifier
L:838 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36
M:340 Repeated in SeqNo=36
L:909 M:283 W: Missing Blank Line separator, <400> field identifier
L:911 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:40
L:928 M:283 W: Missing Blank Line separator, <400> field identifier
L:930 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:41
M:340 Repeated in SeqNo=41
L:1033 M:283 W: Missing Blank Line separator, <400> field identifier
L:1041 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:47
M:340 Repeated in SeqNo=47
L:1124 M:283 W: Missing Blank Line separator, <400> field identifier
L:1132 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:52
L:1143 M:283 W: Missing Blank Line separator, <400> field identifier
L:1145 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:53
M:340 Repeated in SeqNo=53
L:1162 M:283 W: Missing Blank Line separator, <400> field identifier
L:1164 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:54
M:340 Repeated in SeqNo=54
L:1339 M:283 W: Missing Blank Line separator, <400> field identifier
L:1341 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:64
M:340 Repeated in SeqNo=64
L:1376 M:283 W: Missing Blank Line separator, <400> field identifier
L:1378 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:66
L:1505 M:283 W: Missing Blank Line separator, <400> field identifier
L:1509 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:73
L:1568 M:283 W: Missing Blank Line separator, <400> field identifier
L:1572 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:77
M:340 Repeated in SeqNo=77

```
VERIFICATION SUMMARY                    DATE: 07/06/2000
PATENT APPLICATION:  US/09/233,218A      TIME: 13:06:43

Input Set : A:\Tetrapyrole-15090-B.txt
Output Set: N:\CRF3\07062000\I233218A.raw
```

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L:1739 M:283 W: Missing Blank Line separator, <400> field identifier
L:1743 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:87
M:340 Repeated in SeqNo=87
L:1798 M:283 W: Missing Blank Line separator, <400> field identifier
L:1806 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:90
L:1871 M:283 W: Missing Blank Line separator, <400> field identifier
L:1873 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:94
L:1908 M:283 W: Missing Blank Line separator, <400> field identifier
L:1910 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:96
M:340 Repeated in SeqNo=96
L:1927 M:283 W: Missing Blank Line separator, <400> field identifier
L:1929 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:97
M:340 Repeated in SeqNo=97
L:1974 M:283 W: Missing Blank Line separator, <400> field identifier
L:1976 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:100
M:340 Repeated in SeqNo=100
L:2063 M:283 W: Missing Blank Line separator, <400> field identifier
L:2065 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:105
M:340 Repeated in SeqNo=105
L:2210 M:283 W: Missing Blank Line separator, <400> field identifier
L:2212 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:113
M:340 Repeated in SeqNo=113
L:2347 M:283 W: Missing Blank Line separator, <400> field identifier
L:2384 M:283 W: Missing Blank Line separator, <400> field identifier
L:2421 M:283 W: Missing Blank Line separator, <400> field identifier
L:2452 M:283 W: Missing Blank Line separator, <400> field identifier
L:2483 M:283 W: Missing Blank Line separator, <400> field identifier
L:2554 M:283 W: Missing Blank Line separator, <400> field identifier
L:2591 M:283 W: Missing Blank Line separator, <400> field identifier
L:2632 M:283 W: Missing Blank Line separator, <400> field identifier
L:2811 M:283 W: Missing Blank Line separator, <400> field identifier
L:2830 M:283 W: Missing Blank Line separator, <400> field identifier
L:2925 M:283 W: Missing Blank Line separator, <400> field identifier
L:3016 M:283 W: Missing Blank Line separator, <400> field identifier
L:3035 M:283 W: Missing Blank Line separator, <400> field identifier
L:3152 M:283 W: Missing Blank Line separator, <400> field identifier
L:3171 M:283 W: Missing Blank Line separator, <400> field identifier
L:3282 M:283 W: Missing Blank Line separator, <400> field identifier
L:3317 M:283 W: Missing Blank Line separator, <400> field identifier
L:3406 M:283 W: Missing Blank Line separator, <400> field identifier
L:3445 M:283 W: Missing Blank Line separator, <400> field identifier
L:3610 M:283 W: Missing Blank Line separator, <400> field identifier
```